

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/789,526A

Source: JFW/LG

Date Processed by STIC: 9/19/06

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 09/19/2006

PATENT APPLICATION: US/10/789,526A

TIME: 13:18:04

Input Set : A:\PTO.SS.txt

Output Set: N:\CRF4\09192006\J789526A.raw

3 <110> APPLICANT: George Tachas
 4 Kenneth W. Dobie
 5 Ravi Jain
 6 Christopher Ian Belyea
 7 Mark Andrew Heffernan
 9 <120> TITLE OF INVENTION: MODULATION OF GROWTH HORMONE RECEPTOR EXPRESSION AND
 10 INSULIN LIKE GROWTH FACTOR EXPRESSION
 12 <130> FILE REFERENCE: BIOL0002US
 14 <140> CURRENT APPLICATION NUMBER: 10/789,526A
 15 <141> CURRENT FILING DATE: 2004-02-26
 17 <150> PRIOR APPLICATION NUMBER: 60/451,455
 18 <151> PRIOR FILING DATE: 2003-02-28
 20 <160> NUMBER OF SEQ ID NOS: 272
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 20
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Artificial Sequence
 28 <220> FEATURE:
 30 <223> OTHER INFORMATION: Antisense Oligonucleotide
 32 <400> SEQUENCE: 1
 33 tccgtcatcg ctcctcaggg 20
 36 <210> SEQ ID NO: 2
 37 <211> LENGTH: 20
 38 <212> TYPE: DNA
 39 <213> ORGANISM: Artificial Sequence
 41 <220> FEATURE:
 43 <223> OTHER INFORMATION: Antisense Oligonucleotide
 45 <400> SEQUENCE: 2
 46 gtgcgcgcga gcccgaaatc 20
 49 <210> SEQ ID NO: 3
 50 <211> LENGTH: 20
 51 <212> TYPE: DNA
 52 <213> ORGANISM: Artificial Sequence
 54 <220> FEATURE:
 56 <223> OTHER INFORMATION: Antisense Oligonucleotide
 58 <400> SEQUENCE: 3
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 63 <211> LENGTH: 4414
 64 <212> TYPE: DNA
 65 <213> ORGANISM: H. sapiens
 67 <220> FEATURE:
 69 <220> FEATURE:

(pg. 6-7)

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71 <222> LOCATION: (44)...(1960)
73 <400> SEQUENCE: 4
74 ccgcgcctctc tgatcagagg cgaagctcgg aggtcctaca ggt atg gat ctc tgg      55
75                                     Met Asp Leu Trp
76                                     1
78 cag ctg ctg ttg acc ttg gca ctg gca gga tca agt gat gct ttt tct      103
79 Gln Leu Leu Leu Thr Leu Ala Leu Ala Gly Ser Ser Asp Ala Phe Ser
80   5          10          15          20
82 gga agt gag gcc aca gca gct atc ctt agc aga gca ccc tgg agt ctg      151
83 Gly Ser Glu Ala Thr Ala Ala Ile Leu Ser Arg Ala Pro Trp Ser Leu
84          25          30          35
86 caa agt gtt aat cca ggc cta aag aca aat tct tct aag gag cct aaa      199
87 Gln Ser Val Asn Pro Gly Leu Lys Thr Asn Ser Ser Lys Glu Pro Lys
88          40          45          50
90 ttc acc aag tgc cgt tca cct gag cga gag act ttt tca tgc cac tgg      247
91 Phe Thr Lys Cys Arg Ser Pro Glu Arg Glu Thr Phe Ser Cys His Trp
92          55          60          65
94 aca gat gag gtt cat cat ggt aca aag aac cta gga ccc ata cag ctg      295
95 Thr Asp Glu Val His His Gly Thr Lys Asn Leu Gly Pro Ile Gln Leu
96          70          75          80
98 ttc tat acc aga agg aac act caa gaa tgg act caa gaa tgg aaa gaa      343
99 Phe Tyr Thr Arg Arg Asn Thr Gln Glu Trp Thr Gln Glu Trp Lys Glu
100  85          90          95          100
102 tgc cct gat tat gtt tct gct ggg gaa aac agc tgt tac ttt aat tca      391
103 Cys Pro Asp Tyr Val Ser Ala Gly Glu Asn Ser Cys Tyr Phe Asn Ser
104          105          110          115
106 tcg ttt acc tcc atc tgg ata cct tat tgt atc aag cta act agc aat      439
107 Ser Phe Thr Ser Ile Trp Ile Pro Tyr Cys Ile Lys Leu Thr Ser Asn
108          120          125          130
110 ggt ggt aca gtg gat gaa aag tgt ttc tct gtt gat gaa ata gtg caa      487
111 Gly Gly Thr Val Asp Glu Lys Cys Phe Ser Val Asp Glu Ile Val Gln
112          135          140          145
114 cca gat cca ccc att gcc ctc aac tgg act tta ctg aac gtc agt tta      535
115 Pro Asp Pro Pro Ile Ala Leu Asn Trp Thr Leu Leu Asn Val Ser Leu
116          150          155          160
118 act ggg att cat gca gat atc caa gtg aga tgg gaa gca cca cgc aat      583
119 Thr Gly Ile His Ala Asp Ile Gln Val Arg Trp Glu Ala Pro Arg Asn
120 165          170          175          180
122 gca gat att cag aaa gga tgg atg gtt ctg gag tat gaa ctt caa tac      631
123 Ala Asp Ile Gln Lys Gly Trp Met Val Leu Glu Tyr Glu Leu Gln Tyr
124          185          190          195
126 aaa gaa gta aat gaa act aaa tgg aaa atg atg gac cct ata ttg aca      679
127 Lys Glu Val Asn Glu Thr Lys Trp Lys Met Met Asp Pro Ile Leu Thr
128          200          205          210
130 aca tca gtt cca gtg tac tca ttg aaa gtg gat aag gaa tat gaa gtg      727
131 Thr Ser Val Pro Val Tyr Ser Leu Lys Val Asp Lys Glu Tyr Glu Val
132          215          220          225
134 cgt gtg aga tcc aaa caa cga aac tct gga aat tat ggc gag ttc agt      775

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135 Arg Val Arg Ser Lys Gln Arg Asn Ser Gly Asn Tyr Gly Glu Phe Ser
136      230      235      240
138 gag gtg ctc tat gta aca ctt cct cag atg agc caa ttt aca tgt gaa      823
139 Glu Val Leu Tyr Val Thr Leu Pro Gln Met Ser Gln Phe Thr Cys Glu
140 245      250      255      260
142 gaa gat ttc tac ttt cca tgg ctc tta att att atc ttt gga ata ttt      871
143 Glu Asp Phe Tyr Phe Pro Trp Leu Leu Ile Ile Ile Phe Gly Ile Phe
144      265      270      275
146 ggg cta aca gtg atg cta ttt gta ttc tta ttt tct aaa cag caa agg      919
147 Gly Leu Thr Val Met Leu Phe Val Phe Leu Phe Ser Lys Gln Gln Arg
148      280      285      290
150 att aaa atg ctg att ctg ccc cca gtt cca gtt cca aag att aaa gga      967
151 Ile Lys Met Leu Ile Leu Pro Pro Val Pro Val Pro Lys Ile Lys Gly
152      295      300      305
154 atc gat cca gat ctc ctc aag gaa gga aaa tta gag gag gtg aac aca      1015
155 Ile Asp Pro Asp Leu Leu Lys Glu Gly Lys Leu Glu Glu Val Asn Thr
156      310      315      320
158 atc tta gcc att cat gat agc tat aaa ccc gaa ttc cac agt gat gac      1063
159 Ile Leu Ala Ile His Asp Ser Tyr Lys Pro Glu Phe His Ser Asp Asp
160 325      330      335      340
162 tct tgg gtt gaa ttt att gag cta gat att gat gag cca gat gaa aag      1111
163 Ser Trp Val Glu Phe Ile Glu Leu Asp Ile Asp Glu Pro Asp Glu Lys
164      345      350      355
166 act gag gaa tca gac aca gac aga ctt cta agc agt gac cat gag aaa      1159
167 Thr Glu Glu Ser Asp Thr Asp Arg Leu Leu Ser Ser Asp His Glu Lys
168      360      365      370
170 tca cat agt aac cta ggg gtg aag gat ggc gac tct gga cgt acc agc      1207
171 Ser His Ser Asn Leu Gly Val Lys Asp Gly Asp Ser Gly Arg Thr Ser
172      375      380      385
174 tgt tgt gaa cct gac att ctg gag act gat ttc aat gcc aat gac ata      1255
175 Cys Cys Glu Pro Asp Ile Leu Glu Thr Asp Phe Asn Ala Asn Asp Ile
176      390      395      400
178 cat gag ggt acc tca gag gtt gct cag cca cag agg tta aaa ggg gaa      1303
179 His Glu Gly Thr Ser Glu Val Ala Gln Pro Gln Arg Leu Lys Gly Glu
180 405      410      415      420
182 gca gat ctc tta tgc ctt gac cag aag aat caa aat aac tca cct tat      1351
183 Ala Asp Leu Leu Cys Leu Asp Gln Lys Asn Gln Asn Asn Ser Pro Tyr
184      425      430      435
186 cat gat gct tgc cct gct act cag cag ccc agt gtt atc caa gca gag      1399
187 His Asp Ala Cys Pro Ala Thr Gln Gln Pro Ser Val Ile Gln Ala Glu
188      440      445      450
190 aaa aac aaa cca caa cca ctt cct act gaa gga gct gag tca act cac      1447
191 Lys Asn Lys Pro Gln Pro Leu Pro Thr Glu Gly Ala Glu Ser Thr His
192      455      460      465
194 caa gct gcc cat att cag cta agc aat cca agt tca ctg tca aac atc      1495
195 Gln Ala Ala His Ile Gln Leu Ser Asn Pro Ser Ser Leu Ser Asn Ile
196      470      475      480
198 gac ttt tat gcc cag gtg agc gac att aca cca gca ggt agt gtg gtc      1543
199 Asp Phe Tyr Ala Gln Val Ser Asp Ile Thr Pro Ala Gly Ser Val Val

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202	ctt	tcc	ccg	ggc	caa	aag	aat	aag	gca	ggg	atg	tcc	caa	tgt	gac	atg	1591
203	Leu	Ser	Pro	Gly	Gln	Lys	Asn	Lys	Ala	Gly	Met	Ser	Gln	Cys	Asp	Met	
204					505					510					515		
206	cac	ccg	gaa	atg	gtc	tca	ctc	tgc	caa	gaa	aac	ttc	ctt	atg	gac	aat	1639
207	His	Pro	Glu	Met	Val	Ser	Leu	Cys	Gln	Glu	Asn	Phe	Leu	Met	Asp	Asn	
208					520					525					530		
210	gcc	tac	ttc	tgt	gag	gca	gat	gcc	aaa	aag	tgc	atc	cct	gtg	gct	cct	1687
211	Ala	Tyr	Phe	Cys	Glu	Ala	Asp	Ala	Lys	Lys	Cys	Ile	Pro	Val	Ala	Pro	
212					535					540					545		
214	cac	atc	aag	gtt	gaa	tca	cac	ata	cag	cca	agc	tta	aac	caa	gag	gac	1735
215	His	Ile	Lys	Val	Glu	Ser	His	Ile	Gln	Pro	Ser	Leu	Asn	Gln	Glu	Asp	
216					550					555					560		
218	att	tac	atc	acc	aca	gaa	agc	ctt	acc	act	gct	gct	ggg	agg	cct	ggg	1783
219	Ile	Tyr	Ile	Thr	Thr	Glu	Ser	Leu	Thr	Thr	Ala	Ala	Gly	Arg	Pro	Gly	
220						570					575					580	
222	aca	gga	gaa	cat	gtt	cca	ggt	tct	gag	atg	cct	gtc	cca	gac	tat	acc	1831
223	Thr	Gly	Glu	His	Val	Pro	Gly	Ser	Glu	Met	Pro	Val	Pro	Asp	Tyr	Thr	
224					585					590					595		
226	tcc	att	cat	ata	gta	cag	tcc	cca	cag	ggc	ctc	ata	ctc	aat	gcg	act	1879
227	Ser	Ile	His	Ile	Val	Gln	Ser	Pro	Gln	Gly	Leu	Ile	Leu	Asn	Ala	Thr	
228					600					605					610		
230	gcc	ttg	ccc	ttg	cct	gac	aaa	gag	ttt	ctc	tca	tca	tgt	ggc	tat	gtg	1927
231	Ala	Leu	Pro	Leu	Pro	Asp	Lys	Glu	Phe	Leu	Ser	Ser	Cys	Gly	Tyr	Val	
232					615					620					625		
234	agc	aca	gac	caa	ctg	aac	aaa	atc	atg	cct	tag	cctttctttg	gtttcccaag				1980
235	Ser	Thr	Asp	Gln	Leu	Asn	Lys	Ile	Met	Pro							
236					630					635							
238	agctacgtat	ttaatagcaa	agaattgact	ggggcaataa	cgtttaagcc	aaaacaatgt											2040
240	ttaaacccttt	tttgggggag	tgacaggatg	gggtatggat	tctaaaatgc	cttttcccaa											2100
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244	tgtgcaatgt	aaatatttta	aagaattgtg	tcagactggt	tagtagcagt	gattgtctta											2220
246	atattgtggg	tgtaattttt	tgatactaag	cattgaatgg	ctatgttttt	aatgtatagt											2280
248	aatcacgct	ttttgaaaaa	gcgaaaaaat	caggtggctt	ttgcggttca	ggaaaattga											2340
250	atgcaaacca	tagcacaggc	taattttttg	ttgtttctta	aataagaaac	ttttttattt											2400
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254	ggatatgtaa	aacattttact	ttgacataaa	gttgataaag	attttttaat	aatttagact											2520
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262	taaaatgatt	gtagtaatct	gcattatttg	aatataattg	ttttatctga	atttttaaac											2760
264	aagtatttgt	taatttagaa	aactttaaag	cgtttgcaca	gatcaactta	ccaggcacca											2820
266	aaagaagtaa	aagcaaaaaa	gaaaaccttt	cttcaccaa	tcttggttga	tgccaaaaaa											2880
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270	gctgcaattg	cacgcggagt	gagtttttta	gtgcgtgcag	atggtgagag	ataagatcta											3000
272	tagcctctgc	agcggaatct	gttcacaccc	aacttggttt	tgctacataa	ttatccagga											3060
274	aggggaataag	gtacaagaag	cattttgtta	gttgaagcaa	atcgaatgaa	attaactggg											3120
276	taatgaaaca	aagagttcaa	gaaataagtt	tttgtttcac	agcctataac	cagacacata											3180
278	ctcatttttc	atgataatga	acagaacata	gacagaagaa	acaaggtttt	cagtccccac											3240

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280 agataactga aaattattta aaccgctaaa agaaactttc tttctcacta aatcttttat 3300
282 aggattttatt taaaatagca aaagaagaag tttcatcatt ttttacttcc tctctgagtg 3360
284 gactggcctc aaagcaagca ttcagaagaa aaagaagcaa cctcagtaat ttagaaatca 3420
286 ttttgcaatc ccttaatatc ctaaacatca ttcatttttg ttggtgtgtg ttggtgtgag 3480
288 acagagtctc gctctgtcgc caggctagag tgcggtggcg cgatcttgac tcaactgcaat 3540
290 ctccacctcc cacaggttca ggcgattccc gtgcctcagc ctcttgagta gctgggacta 3600
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300 cttctcattt tttaaaaaag cttaaaactt tgaagttagc ttttaactta atagtatttc 3900
302 ccatttatcg cagacctttt ttaggaagca agcttaatgg ctgataattt taaattctct 3960
304 ctcttgagg aaggactatg aaaagctaga attgagtggt taaagttcaa catgttattt 4020
306 gtaatagatg tttgatagat tttctgctac tttgctgcta tggttttctc caagagctac 4080
308 ataatttagt ttcataataa gtatcatcag tgtagaacct aattcaattc aaagctgtgt 4140
310 gtttggaaga ctatcttact atttcacaac agcctgacaa catttctata gccaaaaata 4200
312 gctaaatacc tcaatcagtc tcagaatgtc attttggtac tttggtggcc acataagcca 4260
314 ttattcacta gtatgactag ttgtgtctgg cagtttatat ttaactctct ttatgtctgt 4320
316 ggattttttc cttcaaagtt taataaattt attttcttgg attcctgata atgtgcttct 4380
318 gttatcaaac accaacataa aaatgatcta aacc 4414

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321 <210> SEQ ID NO: 5

322 <211> LENGTH: 21

323 <212> TYPE: DNA

324 <213> ORGANISM: Artificial Sequence

326 <220> FEATURE:

328 <223> OTHER INFORMATION: PCR Primer

330 <400> SEQUENCE: 5

331 gatgtcccaa tgtgacatgc a 21

334 <210> SEQ ID NO: 6

335 <211> LENGTH: 26

336 <212> TYPE: DNA

337 <213> ORGANISM: Artificial Sequence

339 <220> FEATURE:

341 <223> OTHER INFORMATION: PCR Primer

343 <400> SEQUENCE: 6

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347 <210> SEQ ID NO: 7

348 <211> LENGTH: 26

349 <212> TYPE: DNA

350 <213> ORGANISM: Artificial Sequence

352 <220> FEATURE:

354 <223> OTHER INFORMATION: PCR Probe

356 <400> SEQUENCE: 7

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360 <210> SEQ ID NO: 8

361 <211> LENGTH: 19

362 <212> TYPE: DNA

363 <213> ORGANISM: Artificial Sequence

365 <220> FEATURE:

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:100; N Pos. 25945,25946,25947,25948,25949,25950,25951,25952,25953
Seq#:100; N Pos. 25954,25955,25956,25957,25958,25959,25960,25961,25962
Seq#:100; N Pos. 25963,25964,25965,25966,25967,25968,25969,25970,25971
Seq#:100; N Pos. 25972,25973,25974,25975,25976,25977,25978,25979,25980
Seq#:100; N Pos. 25981,25982,25983,25984,25985,25986,25987,25988,25989
Seq#:100; N Pos. 25990,25991,25992,25993,25994,25995,25996,25997,25998

VERIFICATION SUMMARY

DATE: 09/19/2006

PATENT APPLICATION: US/10/789,526A

TIME: 13:18:05

Input Set : A:\PTO.SS.txt

Output Set: N:\CRF4\09192006\J789526A.raw

L:654 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:2632
M:341 Repeated in SeqNo=11
L:3137 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:98 after pos.:2400
M:341 Repeated in SeqNo=98
L:3336 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:99 after pos.:2460
M:341 Repeated in SeqNo=99
L:3426 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:100 after pos.:0
M:341 Repeated in SeqNo=100